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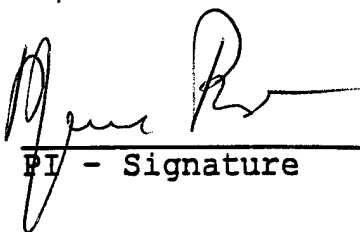
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# 1 Introduction

The problem of image registration is encountered in various applications, from stereo imaging to medical imaging. A class of registration problems involves rigid objects and at least partial knowledge about acquisition conditions and the objective is to establish matches between features (points or group of points). In these cases, complete matching is achieved through 3-D model building and interpolation, e.g., [6],[7]. In alternative problems, the objective is to match nonrigid objects which in simpler cases consist of rigid components whose relative positions can be freely changed, e.g., [10]. In other cases, the objects are elastic and deformable, e.g., human face or body parts and the objective is to establish correspondence between meaningful subparts; most frequently such problems are encountered in medicine and human gesture recognition. Registration may be achieved by elastic model-based matching, e.g., matching between brain images and medical atlas described in [1]. Alternatively, different views may be used to build a 3-D model, an example of the approach is model building using a sequence of stomach X-ray images acquired under different view and under physical deformation, [9].

The objective of the registration proposed in this work is to provide for comparison between temporally spaced mammograms of a patient with the objective of detecting early cancerous signs. The objective, as well as, physical characteristics of the breast tissue differ from other problems of medical image registration and thus it is necessary to develop a different approach. Mammogram acquisition involves compression of elastic breast tissue and the resulting images contain superimposed breast tissue components. The primary components of a breast are fatty and fibro-glandular tissues and the ratio of the two varies from individual to individual and changes over time (in favor of the fatty component). In addition, blood vessels transect breast tissue. Radiologically, fatty tissue is radiolucent and fibro-glandular radiopaque; both

are characterized primarily by weakly structured texture. The only elements showing structural properties are blood vessels and ducts (part of glandular tissue). Consequently, a typical mammogram has no identifiable landmark points. Two mammograms (of the same patient and the same breast) acquired in different screenings differ primarily due to the fact that there are variations in positioning and compression. These variations are in essence changes in viewpoint and due to lack of knowledge about the 3-D object characteristics and uncertainty in acquisition parameters it is intractable to establish pixel-to-pixel correspondence. Warping techniques can map a mammogram pair onto each other (see [11]) however, the required interpolation may obscure minor changes which are indicative of early cancer. The concentration of this work is on developing an alternative to precise mammogram registration by defining corresponding regions in two images, as is done by medical experts. These regions can then be analyzed for changes indicative of cancer.

From the technical point of view, regional registration of mammograms is the problem of identifying similar regions in weakly structured texture patterns. In the proposed approach a mammogram pair is covered by corresponding circles of varying radii. The circles may overlap but there are no gaps in either image. The locations of the centers of corresponding circles are determined relative to a small set of identifiable points and the radius of each pair is determined by intensity characteristics of the older mammogram. Detection and correspondence between the identifiable points, also referred to as the control points, is discussed in detail in the last year's report, [4]; the focus of this report is on the determination of corresponding regions. The overall approach, analysis of intensity characteristics and mammogram covering are discussed in Section 2. Section 3 concentrates on the evaluation of the approach.

## 2 Approach

The corresponding regions are selected based on the control points and similarity of texture characteristics. In the present research the regions are circular. The circular geometry is selected because it is invariant to rotational misalignments arising from image digitization (the images are obtained by digitizing film) and requires determining only the corresponding centers and radii. The essential elements of the procedure are illustrated in Figure 1, and they involve the following.

- *Determining the extent of corresponding regions* The radii of the corresponding regions are the same and are determined so that the corresponding regions have similar texture characteristics (this is important for the comparison paradigm). Partitioning of the older mammogram is used to ensure that each region is characterized by a predominantly homogeneous intensity pattern.
- *Covering of a mammogram pair* The covering algorithm generates corresponding circular regions and covers an image pair with overlapping circles with no gaps. The distances between landmark points are used to determine the centers and the radius for each pair is such that it ensures that the region in the older mammogram belongs predominantly to a single partition. Since the distances between control points are not guaranteed to be preserved in two screenings, the region centers are determined as the cluster centers of points obtained by considering all pairwise combinations of matched control points.

### 2.1 Defining region extent

Partitioning employs a hierarchical region growing paradigm that uses pyramidal multiresolution image representation. Relationships between pixels at different resolutions are established by a fuzzy membership function as described in [3]. The

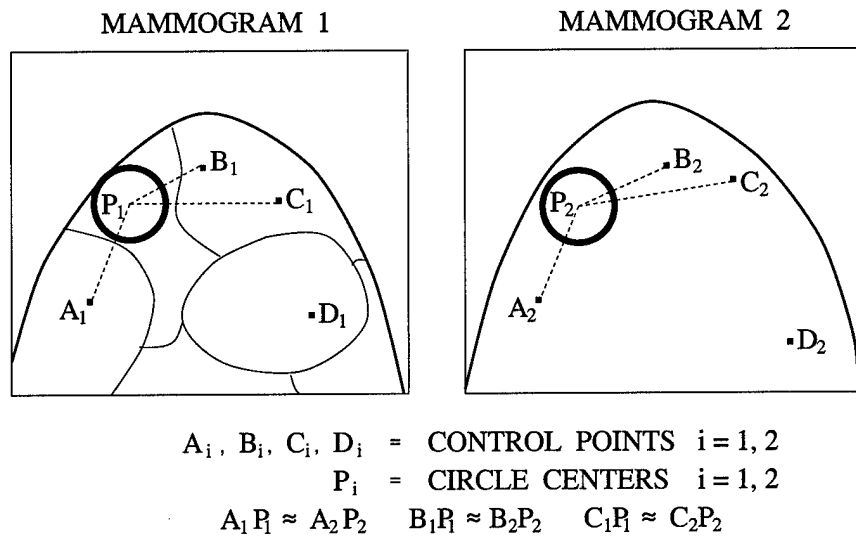


Figure 1: Regional correspondence between mammograms: illustration of procedure.



selection of the parameters of the fuzzy membership function allows for fine-tuning the method to specific segmentation objectives. Additional criteria may be used to limit a region extent, e.g., regions may be limited to a specific size dictated by the spatial resolution and expected types of cancerous changes.

The objective of mammogram partitioning is to segment a mammogram into statistically homogeneous regions with respect to intensity patterns. Highly textured mammogram images dictate the selection of segmentation methods that are successful in dealing with texture regions. Guided by our previous experience, we have chosen the fuzzy pyramid linking method, [3]. The essence of the method is hierarchical region growing that uses pyramidal multiresolution image representation. Relationships between pixels at different resolution levels are established by a fuzzy membership function. The selection of the parameters of the fuzzy membership function allows for fine-tuning the method to specific segmentation objectives. We point out that fuzzy pyramid linking typically results in a large number of regions (about 2000 per mammogram). Only a few of them (typically 5-7) are large enough for further consideration. Large regions typically comprise about 90% of the mammogram. Small regions (for resolution used in this study, below 500 pixels) are mostly distributed along the borders of the larger regions and are merged together with the largest neighboring region.

### 2.1.1 Fuzzy pyramid linking

An image pyramid is a convenient and efficient representation of an image at multiple resolutions. It is created by using the original image  $I_0$  of dimensions  $2^n \times 2^n$  as the base of the pyramid. Each subsequent level of the pyramid,  $I_1 \dots I_n$ , is a square array which is half the dimensions of its predecessor. These arrays are lower resolution representations of the original image. The top level  $I_n$  of the pyramid is a  $1 \times 1$  array. An element (node) of the array  $I_l$  ( $l > 0$ ) is obtained by a weighted averaging of

$I_{l-1}$  nodes within a  $k \times k$  neighborhood, typically  $k = 4$ . A pyramid is created using a specific weighting scheme. A convenient approach to selecting weights is to use a Gaussian weighted averaging technique, as was done in this work. The image pyramid thus created is known as a Gaussian pyramid, [5].

Linking is the process by which the nodes belonging to a given level of the pyramid are connected with nodes at adjacent levels, i.e., links establish relationships between pixels at different resolutions. Links are first used to redefine the pyramid iteratively, and next to segment the image by replacing nodes at level  $l - 1$  by nodes at level  $l$ . Since each Gaussian pyramid level is created by convolving the  $4 \times 4$  weight mask with the preceding level of the pyramid, there exists a predetermined spatial relationship between nodes at two adjacent levels. Each node at level  $l$ ,  $l > 0$ , has a  $4 \times 4$  array of candidate son nodes at level  $l - 1$ . Conversely, for each node at level  $l$ ,  $l < n - 1$ , there exists a  $2 \times 2$  array of candidate father nodes at level  $l + 1$ . The links are established for all son nodes in the pyramid starting with the base of the pyramid and using an algorithm. The pyramid is redefined iteratively and new links are determined. The pyramid structure converges once the links within the pyramid stabilize. Image segmentation can be achieved upon convergence by mapping the lower resolution image at the apex of the pyramid onto the original image at the base of the pyramid by following the linking paths through the intermediate levels.

A number of proposed linking algorithms link a son node to the father node that is the most similar based on a chosen property, e.g., intensity. These algorithms are frequently referred to as hard linking. In contrast, in this paper we propose a different algorithm where a son node is linked to all four candidate father nodes. This algorithm differs from the hard linking in that it allows connections between intensities that differ significantly and the strength of the link is a function of the absolute difference between the value of a son node and its candidate father node. The linking algorithm used in this work is detailed in the following.

In the proposed algorithm, the following variables are defined for linking and ensuing iterative pyramid redefining process:

- $t_l(i, j)$ : the *local image property* (in this paper intensity);
- $p_l(i, j)$ : the *pointer* to the node's father one level above having the maximum link strength (hereafter referred to *the maximum link*);
- $s_l(i, j)$ : the *strength value of the link* between the father and the son nodes.

The iterations proceed in the following manner:

1. For level  $l = 0$  set

$$s_0(i, j) = 1 \quad \text{and} \quad t_0(i, j) = I_0(i, j).$$

2. For each level  $l$  from 1 to  $n - 1$  set

$$s_l(i, j) = \sum_{i', j'} s_{l-1}(i', j') \phi_{i, j, i', j'},$$

where  $\phi_{i, j, i', j'}$  denotes the strength of the link between the node  $(i, j)$  at level  $l$  and it's son  $(i', j')$  at level  $l - 1$ ,

and

$$t_l(i, j) = \sum_{i', j'} t_{l-1}(i', j') \phi_{i, j, i', j'},$$

with summations performed over all sons of the node.

3. For each node at level  $l$ , for  $0 \leq l < n - 2$ , the pointer  $p_l(i, j)$  points to the father node at level  $l + 1$  that has the maximum link strength among the four candidate father nodes. If two or more fathers have the same link strength, a link is chosen randomly; however, if either link existed in the previous iteration, the link remains unchanged.

4. Once the links have propagated to the top of the pyramid the value of every node, except those at level 0, is recomputed in the following manner:

$$I_l(i, j) = t_l(i, j) / s_l(i, j) \quad \text{for } s_l(i, j) > 0.$$

5. If no link is reassigned during the current iteration, it is assumed that a steady state has been reached. If any number of links have been reassigned during the current iteration, the procedure is repeated starting from step 2.

Upon reaching steady state, image segmentation is achieved in one top-down pass beginning from level  $n - 1$ . In this pass, a son node at level  $l$  is replaced by the father node pointed at by  $p_l(i, j)$ . The proposed algorithm limits the propagation of the links for specific nodes by requiring that the links between the son and father nodes (pointed by  $p_l(i, j)$ ) exceed a specified threshold  $\tau$ .

The choice of the function  $\phi$ , representing the strength of the link, determines the flexibility of the pyramid segmentation. We have considered various monotonically decreasing functions for modeling the strength of the link, including the linear-like, sigmoid-like, and fuzzy membership functions. Characteristics of the class of images to be segmented combined with the objective of segmentation determine “the best” type of function. Considering Fisher ratios and false detections, the fuzzy membership function was found to be the most flexible of the three, [12]. The linking algorithm employing this function is appropriately called *fuzzy pyramid linking*.

The fuzzy membership function is widely used in various applications based on fuzzy set theory, [13]. In these applications the objective is to establish imprecise relationships between objects and concepts, as is the case in this work. Therefore, the strength of the link between nodes  $(i, j)$  and  $(i', j')$  is modeled by

$$\phi_{i,j,i',j'}(u; \alpha, \beta, \gamma) = 1 - S(u; \alpha, \beta, \gamma), \quad (1)$$

where

$$S(u; \alpha, \beta, \gamma) = \begin{cases} 0 & \text{for } u \leq \alpha \\ 2 \left( \frac{u-\alpha}{\gamma-\alpha} \right)^2 & \text{for } \alpha \leq u \leq \beta \\ 1 - 2 \left( \frac{u-\gamma}{\gamma-\alpha} \right)^2 & \text{for } \beta \leq u \leq \gamma \\ 1 & \text{for } u \geq \gamma \end{cases} \quad (2)$$

and  $u = |I_l(i, j) - I_{l-1}(i', j')|$ . The parameters  $\alpha$  and  $\gamma$  determine the shape of the function, and  $\beta = \frac{\alpha+\gamma}{2}$ . Values of  $\phi_{i,j,i',j'}$  range between 0 and 1, and assignment of specific values is determined by selection of  $\alpha$  and  $\gamma$ . The roles of these two parameters are discussed in the next section.

The function  $\phi_{i,j,i',j'}$ , described by Equations (1) and (2), makes the proposed pyramid linking method a special case of the fuzzy ISODATA clustering, [12]. Consequently, based on the convergence of the fuzzy ISODATA clustering, [2], the proposed pyramid linking is convergent, [12]. (The relationship between pyramid linking and ISODATA clustering is discussed by Kasif and Rosenfeld, [8].)

### 2.1.2 Parameter selection

The fuzzy pyramid linking parameters are selected in accordance with the following guidelines. The selection of parameter  $\alpha$  is dictated by (i) expected noise level and (ii) minimum contrast,  $\mu_c$ , to be detected. Generally, the parameter  $\alpha$  should satisfy  $\alpha \ll \mu_c$  and it should be larger than the expected variations due to noise. The impact of the parameter  $\gamma$  is significant as it has two effects: (i) it determines the intensity difference beyond which two pixels are unrelated, and (ii) it determines the weight values for son ( $I_l$ ) and father ( $I_{l-1}$ ) nodes satisfying  $\alpha < |I_l - I_{l-1}| < \gamma$ . If  $\gamma$  is chosen close to  $\alpha$ , the fuzzy pyramid linking algorithm approaches hard pyramid linking. Based on the above reasoning, parameter  $\alpha$  is chosen to be 5 and parameter  $\gamma$  is chosen to be 100. The segmentation in all cases starts from the pyramid level whose size is  $2 \times 2$  pixels.

The parameter  $\tau$  is the most critical one as it decides whether a son node can be replaced by a father node in the segmentation procedure. Therefore, it determines the final number of regions in the segmented image since the maximum links whose values are below the threshold value do not propagate down to the base of the pyramid. Generally,  $0 \leq \tau \leq 1$ , and high values of the maximum links are associated with homogeneous regions, while low values appear around edges. Choosing a small  $\tau$  allows practically all links to propagate, thus generating a few regions in a segmented image. On the other hand, a large value of  $\tau$  does not allow most of the maximum links to propagate, and the segmented image resembles the low-pass filtered original image. In this study, parameter  $\tau$  is chosen to be .85; it should be incrementally increased if further region splitting is required. We point out that the region splitting is not achieved exactly and that there may be some changes around borders of newly formed regions. An example mammogram partitioning is shown in Figure 2.

## 2.2 Defining region centers and mammogram covering

The algorithm for establishing compatible regions in mammograms proceeds as follows.

- *Step 1:* Determine control points in two mammograms as described in [4].
- *Step 2:* Partition the old mammogram into homogeneous regions using the procedure described in [3].
- *Step 3:* For each partition from *Step 2* do the following:
  - *Step 3.1* Determine the location and the radius of the maximum circle inscribed into the partition; allow that up to  $p_1\%$  of the circle area may lay outside the partition.
  - *Step 3.2* Delete the maximum circle from the partition.

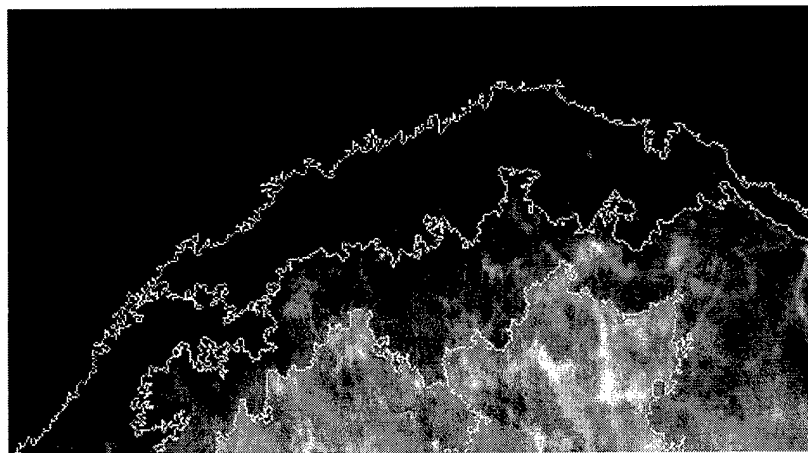


Figure 2: Example of mammogram partitioning (shown is a window of size  $512 \times 512$ ) obtained by the fuzzy pyramid linking algorithm. Partitioning is obtained by segmenting the old mammogram. The region borders are superimposed on the original image to show initial mammogram regions.

- *Step 3.3* Repeat *Step 3.1* and *Step 3.2* until the entire partition is covered; allow for up to  $p_2\%$  overlap between the circles.
- *Step 4:* For each circular region of radius  $R$  centered at  $(x_c^{old}, y_c^{old})$  in the old mammogram determine the compatible circular region of the same radius centered at  $(x_c^{new}, y_c^{new})$  in the new mammogram using the following procedure:
  - *Step 4.1* For a pair of control points in the old mammogram  $(x_1^{old}, y_1^{old})$  and  $(x_2^{old}, y_2^{old})$  and the corresponding pair of control points in the new mammogram  $(x_1^{new}, y_1^{new})$  and  $(x_2^{new}, y_2^{new})$  determine  $(x_c^{new}, y_c^{new})$  as the intersection point of the following two circles<sup>1</sup>

$$(x_1^{new} - x_c^{new})^2 + (y_1^{new} - y_c^{new})^2 = R_1^2 \quad (3)$$

$$(x_2^{new} - x_c^{new})^2 + (y_2^{new} - y_c^{new})^2 = R_2^2, \quad (4)$$

where

$$R_1^2 = (x_1^{old} - x_c^{old})^2 + (y_1^{old} - y_c^{old})^2$$

$$R_2^2 = (x_2^{old} - x_c^{old})^2 + (y_2^{old} - y_c^{old})^2.$$

- *Step 4.2* Repeat *Step 4.1* for each pair of control points in the two mammograms<sup>2</sup>.

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<sup>1</sup>Two circles, in principal, intersect at two points. Only the point that is placed on the same side of the line  $y - y_1^{new} =$

$y \frac{x_2^{new} - x_1^{new}}{x_2^{old} - x_1^{old}}$ , as is the point  $(x_c^{old}, y_c^{old})$  with respect to the line  $y - y_1^{old} = \frac{y_2^{old} - y_1^{old}}{x_2^{old} - x_1^{old}}(x - x_1^{old})$ , is selected; the other point is ignored..

<sup>2</sup>If the number of control points is  $N$ , then *Step 4.1* is repeated  $N(N - 1)/2$  times. This means that ideally  $N(N - 1)/2$  points are determined for  $(x_c^{new}, y_c^{new})$ . However, circles given by Equations (3) and (4) will not always intersect, and this number is less than or equal to  $N(N - 1)/2$ .



- *Step 4.3* Determine the location of the circle center  $(x_2^{new}, y_2^{new})$  by averaging consistent<sup>3</sup> results obtained in *Step 4.2*.

An example of a subset of overlapped circular regions for a mammogram pair is shown in Figure 3.

### 3 Evaluation

Due to difference in compression, breast size may vary in subsequent screenings and consequently it is important to determine the limits of that change for which the algorithm still performs adequately. For that purpose we conducted the following experiment. For a selected mammogram the corresponding deformed mammogram is simulated by scaling, and corresponding circles are determined in the scaled image. Then, the area of the scaled mammogram that is not covered by the circles is measured. The algorithm is said to fail if the uncovered area of the deformed mammogram extends in the breast area determined by the mammogram segmentation. The experiment is performed by changing the parameter  $p_1$  (the area of the circle that may lie outside the partition) from 10% to 40% in increments of 10% and by scaling the original image from 1% to 10% in increments of 1%. In this experiment the parameter  $p_2$  is not critical and is kept fixed at 50%.

The results of the experiment are as follows. For  $p_1 = 10\%$  maximum scaling that can be tolerated is 5%; for  $10\% < p_1 < 40\%$  maximum scaling that can be tolerated can be at least 10%. We did not consider scaling higher than 10%. It should be noted that the larger the  $p_1$ , the larger the number of circular regions and the smaller

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<sup>3</sup>It should be noted that most of the points resulting in *Step 4.2* form a compact cluster. However, occasionally a point or two may drift from the cluster significantly which is particularly noticed in highly distorted mammograms. The points that are far away from the compact cluster may affect the accuracy of determination  $(x_2^{new}, y_2^{new})$  and are excluded from the averaging process.

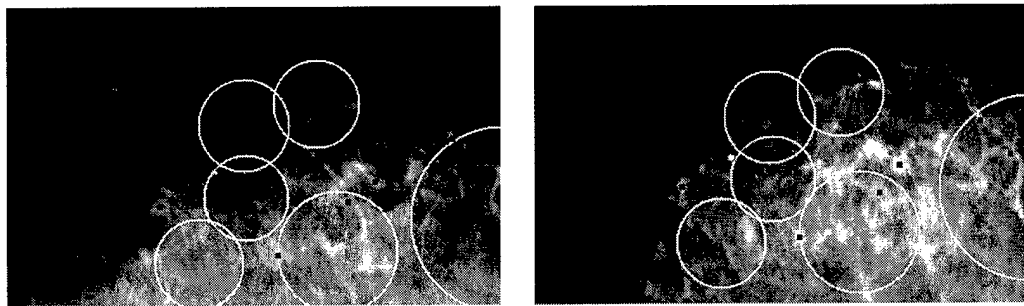


Figure 3: Regional correspondence between mammograms: example of formed circular regions.

the average circle area. In contrast, smaller  $p_1$  produces a smaller number of larger circles. Experimentally, we have determined the value of  $p_1 = 20\%$  as adequate.

### **3.1 Evaluation of the algorithm for establishing compatible regions**

The described algorithm for establishing compatible circular regions in mammograms was tested on 29 mammogram pairs. Depending on the mammogram pair, the segmentation algorithm resulted in between 3 (one pair) and 9 (one pair) initial regions per mammogram, and the majority of the mammograms (16 pairs) were initially segmented into 5 to 7 regions. The size of the initial regions varied from 500 to 30,000 pixels almost uniformly.

The circular regions were formed using  $p_1 = 20\%$  and  $p_2 = 50\%$ . We have not considered circular regions with radii smaller than 10 pixels. Circular regions with radii smaller than 10 pixels are merged with the closest larger neighboring regions.

The results are as follows. The number of circular regions per mammogram varied in the range 15-70. The majority of mammograms contained between 30 and 50 circular regions (23 mammogram pairs). The number of circular regions per mammogram partition varied from 3 to 17 with the typical value of 8-10 (in 70% of all partitions). We have also measured the minimum, maximum, mean, and median circle radius for each considered mammogram pair. These values varied, as shown in Table 1.

The table indicates that minimum and maximum circle radii vary significantly from mammogram to mammogram while the mean and median circle radii are stable. The fact that the median value is slightly smaller than the mean value indicates that a small percentage of circular regions is concentrated below the mean.

It should be noted that due to lack of ground truth the exact evaluation of the position of the established circular regions was not possible. It was, however, verified

	partition (typical)	mammogram (typical)	entire set
minimum radius	10-13	10-13	10-19
maximum radius	varies	50-80	22-88
mean radius	20-30	20-30	15-38
median radius	15-22	15-22	11-37

Table 1: Ranges of values for radii of the established circular regions.

visually that meaningful regions were established in all of the considered mammograms.

## 4 Conclusions

This report discusses formation of corresponding regions in image pairs containing images of elastic bodies characterized by weakly structured texture patterns. The work is motivated by the problem of establishing correspondence between temporally spaced mammograms of the same patient. The proposed approach uses a set of control points and textural characteristics to determine pairs of regions. The approach provides for hierarchical splitting of large regions in order to allow for region comparison at different spatial scales.

The visual evaluation of the proposed algorithms was satisfactory; in addition, the algorithms have successfully passed the tests of handling mammograms where the amount of visible breast tissue differs. The next stage testing is evaluating if established regions are useful in finding suspicious changes, i.e., potential cancerous signs, in the newer mammogram. This work will be subject of a new research project and will be carried out using archived data for which presence of cancer was

established both by mammographers and biopsy.

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